

ABSTRACT

The present invention provides methods for determining the genotype of a nucleic acid at the site of a polymorphism. The methods achieve sensitivities great enough to detect the presence of any difference between the nucleic acids, even single nucleotide polymorphisms. In the methods, the nucleic acid is compared to a reference nucleic acid having a known genotype. The nucleic acids can be of any length, even less than 100 base pairs. In the methods, one or more extra mismatches are introduced into the nucleic acids at or near the site of the polymorphism. The nucleic acids are contacted under conditions in which they are capable of forming a stable four-way complex that can be detected to indicate that the nucleic acids differ in genotype.

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